

IN THE SPECIFICATION

Please replace the paragraph beginning at page 13, line 22 with the following amended paragraph:

Alternatively, a suite of commonly used and free available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at <http://www.ncbi.nlm.nih.gov/BLAST/> ncbi.nlm.nih.gov/BLAST/. The BLAST software suite includes various sequence analysis programs including "blastn," that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at <http://www.ncbi.nlm.nih.gov/gorf/bl2.htm> ncbi.nlm.nih.gov/gorf/bl2.htm. The "BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.12 (April-21-2000) set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Reward for match: 1

Penalty for mismatch: -2

Open Gap: 5 and Extension Gap: 2 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 11

Filter: on

Please replace the paragraph beginning at page 22, line 16 with the following amended paragraph:

Together, Tables 2 and 3 summarize the properties of polypeptides of the invention, and these properties establish that the claimed polypeptides are human cytochrome P450s. For example, SEQ ID NO:1 is 97% identical to a human cytochrome P450 (~~GenBank ID g181382~~) (GenBank ID 181382) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $6.9e-270$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:1 also contains a cytochrome P450 domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:1 is a cytochrome P450. The algorithms and parameters for the analysis of SEQ ID NO:1 are described in Table 7.

Please replace the paragraph beginning at page 52, line 4 with the following amended paragraph:

Transcript images which profile the expression of the polynucleotides of the present invention may also be used in conjunction with in vitro model systems and preclinical evaluation of pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental compounds. All compounds induce characteristic gene expression patterns, frequently termed molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity (Nuwaysir, E.F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and N.L. Anderson (2000) Toxicol. Lett. 112-113:467-471, expressly incorporated by reference herein). If a test compound has a signature similar to that of a compound with known toxicity, it is likely to share those toxic properties. These fingerprints or signatures are most useful and refined when they contain expression information

from a large number of genes and gene families. Ideally, a genome-wide measurement of expression provides the highest quality signature. Even genes whose expression is not altered by any tested compounds are important as well, as the levels of expression of these genes are used to normalize the rest of the expression data. The normalization procedure is useful for comparison of expression data after treatment with different compounds. While the assignment of gene function to elements of a toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not necessary for the statistical matching of signatures which leads to prediction of toxicity. (See, for example, Press Release 00-02 from the National Institute of Environmental Health Sciences, released February 29, 2000, available at <http://www.niehs.nih.gov/oc/news/toxchip.htm> ~~http://www.niehs.nih.gov/oc/news/toxchip.htm~~ [niehs.nih.gov/oc/news/toxchip.htm](http://www.niehs.nih.gov/oc/news/toxchip.htm).) Therefore, it is important and desirable in toxicological screening using toxicant signatures to include all expressed gene sequences.

Please replace the paragraph beginning at page 60, line 33 with the following amended paragraph:

Map locations are represented by ranges, or intervals, of human chromosomes. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Génethon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters. Human genome maps and other resources available to the public, such as the NCBI "GeneMap '99" World Wide Web site (<http://www.ncbi.nlm.nih.gov/genemap/>) (~~http://www.ncbi.nlm.nih.gov/genemap/~~ [ncbi.nlm.nih.gov/genemap/](http://www.ncbi.nlm.nih.gov/genemap/)), can be employed to determine if previously identified disease genes map within or in proximity to the intervals indicated above.

Please amend Tables 1-7, as shown in the attached marked up Tables 1-7, such that Tables 1-7 are numbered as pages 72-79. In addition, please amend Table 2, as shown in the attached marked up Table 2, such that the recitation of GenBank ID "g181382" is replaced with "181382."

Please renumber the pages containing the claims and the abstract as filed (previously pages 72-79) such that the claims and the abstract begin at page 80. Thus, the claims and the abstract will follow Tables 1-7.